Please amend the paragraph that begins at line 4 on page 10 to read as follows:

Orthologs of the disclosed pepper Bs2 protein are typically characterized by possession of at least 50% sequence identity counted over the full length alignment with the amino acid sequence of pepper Bs2 using the NCBI Blast 2.0, gapped blastp set to default parameters. Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, such as at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 90% or at least 95% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs will typically possess at least 75% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85% or at least 90% or 95% depending on their similarity to the reference sequence. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided. The present invention provides not only the peptide homologs are described above, but also nucleic acid molecules that encode such homologs.

A2

Please amend the paragraph that begins at line 6 on page 20 to read as follows:

Variants of the Bs2 protein may also be defined in terms of their sequence identity with the prototype Bs2 protein shown in Seq. ID No. 3. As described above, Bs2 proteins have Bs2 biological activity and share at least 60% sequence identity with the pepper Bs2 protein. Nucleic acid sequences that encode such proteins may readily be determined simply by applying the genetic code to the amino acid sequence of a Bs2 protein, and such nucleic acid molecules may readily be produced by assembling oligonucleotides corresponding to portions of the sequence.

A3

Please amend the paragraph that begins at line 7 on page 20 to read as follows:

To make these transient expression constructs using the *Bs2* gene, adapter primers containing an XbaI site were designed for PCR amplification of the 5' end of the *Bs2* gene. For the X5 construct, the primer was 5' CCTCTAGA**ATGGCTCATGCAAGTGTGCGTTCTCTTATG** 3' (SEQ ID NO: 10) (underlined sequence is the XbaI site, bolded sequence encodes the first 10 amino acids of Bs2). For the XO5 construct which includes the first intron located in the 5' UTR sequence, the primer was 5'CCTCTAGA**C**AAAATATTTCTTGGAGTGAATTTGA 3' (SEQ ID NO: 11) (underlined sequence is the XbaIsite, bolded letter is the transcriptional start site of *Bs2*). For both constructs the second primer used for amplification was 5' CCATCCCACACTTCACAACTCCA 3' (SEQ ID NO: 12). Amplified products were cloned and sequenced to check fidelity of the clones. Clones for both constructs were digested with XbaI and SalI and ligated to pMD1 vector that had been digested with XbaI and SalI. The majority of the *Bs2* gene was isolated as a SalI-EcoRI fragment from a cosmid that was cloned into pBluescript KS + (Stratagene, La Jolla, CA). The 3' ends of the two constructs were derived from PCR amplification of the appropriate 3' RACE product using the primers 5' GTCCTTGAGCGCCTCATG 3' (SEQ ID NO: 13) and 5' ACTAAACTGGGTGTCTCATCGT 3' (SEQ ID NO: 14). This PCR products was cloned into the pCRII-TOPO vector (Invitrogen, Carlsbad, CA) and sequenced to check the fidelity of the clone. The 3' end fragment was isolated by digesting the pCRII-TOPO clone with EcoRI and ligating the fragment to the SalI-EcoRI pBluescript KS + construct that had been digested with EcoRI. Proper orientation of the EcoRI 3' end fragment was determined by sequencing. This construct was digested with SalI and SacI (the SacIsite is in the plasmid polylinker) and ligated to the initial pMD1 constructs which had been digested with SalI and SacI, to produce the X5 and XO5 constructs.